MSRRPWLLALALAVALAAGSAGASTGSDATVPVATQDGPDY
VFHRAHERMLFQTSYTLENNGSVICIPNNGQCFCLAWLKSNG
TNAEKLAANILQWITFALSALCLMFYGYQTWKSTCGWEEIYVA
TIEMIKFIIEYFHEFDEPAVIYSSNGNKTVWLRYAEWLLTCPVILI
HLSNLTGLANDYNKRTMGLLVSDIGTIVWGTTAALSKGYVRVI
FFLMGLCYGIYTFFNAAKVYIEAYHTVPKGICRDLVRYLAWLY
FCSWAMFPVLFLLGPEGFGHINQFNSAIAHAILDLASKNAWS
MMGHFLRVKIHEHILLYGDIRKKQKVNVAGQEMEVETMVHEE
DDETQKVPTAKYANRDSFIIMRDRLKEKGFETRASLDGDPNG
DAEANAAAGGKPGMEMGKMTGMGMGMGAGMGMATIDSGR
VILAVPDISMVDFFREQFARLPVPYELVPALGAENTLQLVQQA
QSLGGCDFVLMHPEFLRDRSPTGLLPRLKMGGQRAAAFGW
AAIGPMRDLIEGSGVDGWLEGPSFGAGINQQALVALINRMQQ
AKKMGMMGGMGMGMGGGMGMGMGMGMGMAPSMNAGM
TGGMGGASMGGAVMGMGMGMQPMQQAMPAMSPMMTQQ
PSMMSQPSAMSAGGAMQAMGGVMPSPAPGGRVGTNPLFG
SAPSPLSSQPGISPGMATPPAATAAPAAGGSEAEMLQQLMS
EINRLKNELGE (SEQ ID NO:1)

Fig. 1A

MDYGGALSAVGRELLFVTNPVVVNGSVLVPEDQCYCAGWIE

SRGTNGAQTASNVLQWLAAGFSILLLMFYAYQTWKSTCGWE

EIYVCAIEMVKVILEFFFEFKNPSMLYLATGHRVQWLRYAEWL

LTCPVILIHLSNLTGLSNDYSRRTMGLLVSDIGTIVWGATSAMA

TGYVKVIFFCLGLCYGANTFFHAAKAYIEGYHTVPKGRCRQV

VTGMAWLFFVSWGMFPILFILGPEGFGVLSVYGSTVGHTIIDL

MSKNCWGLLGHYLRVLIHEHILIHGDIRKTTKLNIGGTEIEVETL

VEDEAEAGAVNKGTGKYASRESFLVMRDKMKEKGIDVRASL

DNSKEVEQEQAARAAMMMMNGNGMGMGMGMNGMNGMG

GMNGMAGGAKPGLELTPQLQPGRVILAVPDISMVDFFREQFA

QLSVTYELVPALGADNTLALVTQAQNLGGVDFVLIHPEFLRDR

SSTSILSRLRGAGQRVAAFGWAQLGPMRDLIESANLDGWLE

GPSFGQGILPAHIVALVAKMQQMRKMQQMQQIGMMTGGMN

GMGGGMGGGMNGMGGGNGMNNMGNGMGGGMGNGMGG

NGMNGMGGGNGMNNMGGNGMAGNGMGGGMGGNGMGG

SMNGMSSGVVANVTPSAAGGMGGMMNGGMAAPQSPGMN

GGRLGTNPLFNAAPSPLSSQLGAEAGMGSMGGMGGMSGM

GGMGGMGGMGGAGAATTQAAGGNAEAEMLQNLMNEINRL

KRELGE (SEQ ID NO: 2)

Fig 1B

MlptavegvsqAQITGRPEWIWLALGTALMGLGTLYFLVKGMGVS

DPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMVPFGGEQNPI

YWARYADWLFTTPLLLLDLALLVDADQGTILALVGADGIMIGT

GLVGALTKVYSYRFVWWAISTAAMLYILYVLFFGFTSKAESMR

PEVASTFKVLRNVTVVLWSAYPVVWLIGSEGAGIVPLNIETLLF

MVLDVSAKVGFGLILLRSRAIFGEAEAPEPSAGDGAAATSD
(SEQ ID NO:3)

Fig. 1C

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Chop1 ..MSRRPWLLALALAVALAAGSAGASTGSDATVPVATQDGPDYVFHRAHFRMFQTSYTLEN 60
Chop2 ...............................MDYGGALSVVGSEILFVTNPVVV 23
Bop   ...................................M

Chop1 ..NGSVICIPNNGCFCLAVLKN---CFAEKFANLCLITFALSAICMYGVQMFWSFC 118
Chop2 ..NGSVL-VEED-CYCAGVIESR---NGAQTSIVLQLAAFSIILMFYACLHSSIC 79
Bop   ..LPTAVEGVSQASITGRPEWIWIALGTALMGLGTLYFLVKGMGVSDPDAKKEYAITLVPA 51

Chop1 ..SAMLVYATIVIKFVIFYFHLDPEAVISSNLSKTVIRLAELFSEVIFHLSMLT 178
Chop2 ..SMFLVYCAIVVVLIFNFNFRKNLSMILATLHRVQFRYLEILLIHLYALT 139
Bop   ..IAFTMYLS-LLGYGLTMVPFGGEQ------NPIYWARYADWLFTTPLLLIDLALLVDA-L 100

Chop1 ..CPANYNKPTLIVSDIGIYFIASCLIMSLLCLIIFFNNAFVV 235
Chop2 ..SLNVSRELLVSDHLWVIALSIMATCVKVLLICIFCSANNHFAV 196
Bop   ..V-DATQGTLIAVGADGIMIGTLVGSYFVWWAISTAAMLILYVLFFGFT 157
```

Fig. 1D

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Fig. 1D (continued)

```
Chop1..GLGMGMG-MAPSMNAPITGMGMG.---AS.G.------AVM.MG.MGMQP.QQAMP--AMSPM 616
Chop2..CG.NGMNNMGNGMGGG.MGNG.GGNGMNGN.GNGMNNMG.GNGMNNNMG.AGNGM.GGG.GGNGNGMGGS 616

Chop1..MTQQP.-MMSQPSAMS.G.GAMQANG.VPS.AP----.GG.VC.TMP.MGS.PS.MSS.--- 667
Chop2..MNGMS.GVVANVTPSA.GGMGGMIN.GMAA.QSPGMNGG.LGTMP.ENA.PS.M.SSO.LGA 676

Chop1..--------------PS.ISPG.ATPP.A.DAAP.AGGSEAR.QQLMSE.MP.IN--M.G.K 712
Chop2..EAGMGSMGGMGGMSGMGGMGG.GGAG.A.TQA.GGNA.A.Q.NLMNF.R.R.R.CH 737
```

(SEQ ID NO: 1)

(SEQ ID NO: 2)

Fig. 1D (continued)

```
....5...10....5...20....5...30....5...40
MDYGGALSAVGRELLFVTNPVVVNGSVLVPEDQCYCAGWI        40
ESRGTNGAQTASNVLQWLAAGFSILLLMFYAYQTWKSTCG        80
WEEIYVCAIEMVKVILEFFFEFKNPSMLYLATGHRVQWLR       120
YAEWLLTCPVILIRLSNLTGLSNDYSRRTMGLLVSDIGTI       160
VWGATSAMATGYVKVIFFCLGLCYGANTFFHAAKAYIEGY       200
HTVPKGRCRQVVTGMAWLFFVSWGMFPILFILGPEGFGVL       240
SVYGSTVGHTIIDLMSKNCWGLLGHYLRVLIHEHILIHGD       280
IRKTTKLNIGGTEIEVETLVEDEAEAGAVNKGTGK (SEQ ID No.4)315
```

Fig. 1E